



Mahidol University
Faculty of Science

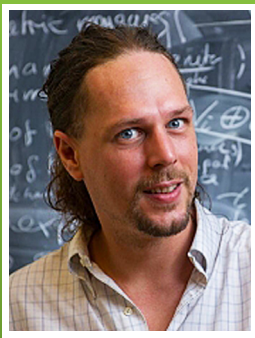
MUSC Research Forum

Monday 18th December 2017

13:30 - 16:00 p.m.

at Room K102, Chalermprakit Building,
Faculty of Science, Mahidol University, Phayathai

All are Welcome



Asst. Prof. Dr. Alexander Bucksch

Department of Plant Biology / Institute of
Bioinformatics / Warnell School of Forestry
and Natural Resources

Schedule

13:30-14:00	Registration
14:00-14:10	Opening Remarks Assist. Prof. Tanakorn Osothchan Deputy Dean for Research, Faculty of Science, Mahidol University
14:10-14:55	Talk by Assistant Professor Dr. Alexander Bucksch
14:55-15:30	Questions & Answers
15:30-16:00	Refreshment & Snack

**“The shape of plants to come: Unleashing topology
and geometry for 21st century plant science”**

The shape of plants encodes information about their growth environment because of their ability to adapt to a range of environments. In particular branching structures of plants are highly plastic and change their shape in response to environmental stresses. We can capture branching structures such as root shapes or tree crowns with various imaging technologies that allow us to mathematically quantify the adaption encoded in the root shape using topological and geometrical techniques ranging derived from a range of mathematics areas such as algebraic topology or computational geometry. In combination with the increasing availability of super-computing technology we are able to analyze thousands of samples in 2D or 3D. As a result, such high-throughput analysis of plant shapes provides new avenues for molecular biologists to achieve the crop yields needed to sustain the projected world population of 11 billion people or equips ecologists with the tools to characterize plant responses to ongoing climate change. In my talk, I will demonstrate emerging trends in shape theory on examples developed by our computational plant science group. The examples will include statistical analysis techniques for shape descriptors applied to crop root systems and tree architectures. The presented descriptors capture the complete branching structure numerically, which allows detailed analysis of the variations of branching architectures within one genotype or the discrimination of hundreds of genotypes. Some of the presented examples will be imaged under field conditions using the currently available DIRT platform as well as first implementations of the upcoming DIRT3D platform. I will also present preliminary results of the Cassava analysis developed in collaboration with researchers at the Roots Lab of Mahidol University.